Cryo-Electron Microscopy: A Revolution in Structural Biology

Nonappa*

Department of Applied Physics, Aalto University, Puumiehenkuja 2, FI-02150, Espoo, Finland.
Email: nonappa@aalto.fi

Abstract: Biomolecules such as proteins and nucleic acids are the fundamental basis for all living organisms. Since the demonstration of first atomic level details of DNA, the field of structural biology has evolved at an unprecedented rate, wherein X-ray crystallography has been the primary tool for atomic level structure determination over the past six decades. X-ray crystallography has been very powerful method, yet limited by the fact that the molecule of interest must be crystallized, which is not always possible especially for biomolecules. Nuclear magnetic resonance (NMR) spectroscopy has been used since 1980s to determine the macromolecular structures in solution. However, NMR is laborious and challenging for large molecules. Simultaneously, electron microscopy (EM) has evolved as one of the important tool in imaging. Even though, the first EM was built in 1930s by Ernst Ruska, the application of EM to achieve atomic level details of biomolecules has appeared in 1970s. The rapid progress in the instrumentation, sample preparation methods such as Cryo-EM and computational power has triggered a revolution in structural biology by simplifying and improving biomolecular imaging. Thanks to the pioneering work of Richard Henderson, Jochim Frank and Jacques Dubochet (Nobel Prize in Chemistry, 2017), today researchers can construct the 3D structures of a range of biomolecules at atomic level resolution, including the recently reported Zika virus. These structures will provide an effective platform to identify/develop new antibiotics and combat some of the deadly diseases. I will present a general over view of the Cryo-electron microscopy and discuss the contribution of this year's Noble Laureates in developing Cryo-EM along with the Finnish contribution in the growth of electron microscopy.